

1636

RAW SEQUENCE LISTING DATE: 07/13/2000
 PATENT APPLICATION: US/08/328,673A TIME: 14:06:16

Input Set : A:\169309-2.app
 Output Set: N:\CRF3\07132000\H328673A.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: Gregory, Richard J.
 7 Wills, Ken N.
 8 Maneval, Daniel C.
 10 (ii) TITLE OF INVENTION: Recombinant Adenoviral Vector and
 11 Methods of Use
 13 (iii) NUMBER OF SEQUENCES: 9
 15 (iv) CORRESPONDENCE ADDRESS:
 16 (A) ADDRESSEE: Townsend and Townsend and Crew LLP
 17 (B) STREET: Two Embarcadero Center, Eighth Floor
 18 (C) CITY: San Francisco
 19 (D) STATE: California
 20 (E) COUNTRY: USA
 21 (F) ZIP: 94111-3834
 23 (v) COMPUTER READABLE FORM:
 24 (A) MEDIUM TYPE: Floppy disk
 25 (B) COMPUTER: IBM PC compatible
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 C--> 29 (vi) CURRENT APPLICATION DATA:
 C--> 30 (A) APPLICATION NUMBER: US/08/328,673A
 C--> 31 (B) FILING DATE: 25-Oct-1994
 32 (C) CLASSIFICATION:
 38 (vii) PRIOR APPLICATION DATA:
 C--> 35 (A) APPLICATION NUMBER: US 08/142,669
 C--> 36 (B) FILING DATE: 25-OCT-1993
 C--> 39 (A) APPLICATION NUMBER: US 08/233,669
 C--> 40 (B) FILING DATE: 26-APR-1994
 42 (viii) ATTORNEY/AGENT INFORMATION:
 43 (A) NAME: Smith, Timothy S.
 44 (B) REGISTRATION NUMBER: 35,367
 45 (C) REFERENCE/DOCKET NUMBER: 016930-000920US
 47 (ix) TELECOMMUNICATION INFORMATION:
 48 (A) TELEPHONE: (415) 576-0200
 49 (B) TELEFAX: (415) 576-0300
 52 (2) INFORMATION FOR SEQ ID NO: 1:
 54 (i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 25 base pairs
 56 (B) TYPE: nucleic acid
 57 (C) STRANDEDNESS: single
 58 (D) TOPOLOGY: linear
 W--> 60 (ii) MOLECULE TYPE: DNA
 63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 65 CGCCACCGAG GGACCTGAGC GAGTC
 68 (2) INFORMATION FOR SEQ ID NO: 2:
 70 (i) SEQUENCE CHARACTERISTICS:

25

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71          (A) LENGTH: 20 base pairs
72          (B) TYPE: nucleic acid
73          (C) STRANDEDNESS: single
74          (D) TOPOLOGY: linear
W--> 76      (ii) MOLECULE TYPE: DNA
79      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
81 TTCTGGGAAG GGACAGAAGA                                20
84 (2) INFORMATION FOR SEQ ID NO: 3:
86      (i) SEQUENCE CHARACTERISTICS:
87          (A) LENGTH: 25 base pairs
88          (B) TYPE: nucleic acid
89          (C) STRANDEDNESS: single
90          (D) TOPOLOGY: linear
W--> 92      (ii) MOLECULE TYPE: DNA
95      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
97 CGCGCTAGCT CTGCCCCAAA GAGCT                            25
100 (2) INFORMATION FOR SEQ ID NO: 4:
102      (i) SEQUENCE CHARACTERISTICS:
103          (A) LENGTH: 39 base pairs
104          (B) TYPE: nucleic acid
105          (C) STRANDEDNESS: single
106          (D) TOPOLOGY: linear
W--> 108     (ii) MOLECULE TYPE: DNA
111     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
113 CGCGGTACCC TCGAGTCTAG ATATTGCCAG TCGTGGAAG           39
116 (2) INFORMATION FOR SEQ ID NO: 5:
118     (i) SEQUENCE CHARACTERISTICS:
119         (A) LENGTH: 35 base pairs
120         (B) TYPE: nucleic acid
121         (C) STRANDEDNESS: single
122         (D) TOPOLOGY: linear
W--> 124     (ii) MOLECULE TYPE: DNA
127     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
129 CGTGCGGCCG CTGGAGGACT TTGAGGATGT CTGTC               35
132 (2) INFORMATION FOR SEQ ID NO: 6:
134     (i) SEQUENCE CHARACTERISTICS:
135         (A) LENGTH: 33 base pairs
136         (B) TYPE: nucleic acid
137         (C) STRANDEDNESS: single
138         (D) TOPOLOGY: linear
W--> 140     (ii) MOLECULE TYPE: DNA
143     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
145 CGCTCTAGAG AGACCAGTTA GGAAGTTTC GCA                   33
148 (2) INFORMATION FOR SEQ ID NO: 7:
150     (i) SEQUENCE CHARACTERISTICS:
151         (A) LENGTH: 2995 base pairs
152         (B) TYPE: nucleic acid
153         (C) STRANDEDNESS: single
154         (D) TOPOLOGY: linear

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156      (ii) MOLECULE TYPE: cDNA
159      (ix) FEATURE:
160          (A) NAME/KEY: CDS
161          (B) LOCATION: 139..2925
162          (D) OTHER INFORMATION: /product= "RB"
163 /note= "retinoblastoma tumor suppressor"
166      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
168      TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTAA CGGGAGTCGG GAGAGGACGG      60
170      GCGGTGCCCC GCGTGC GCGC GCGTCGTCCT CCCGCGCGCT CCTCCACAGC TCGCTGGCTC      120
172      CCGCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC      171
173          Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
174          1 5 10
176      ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCC      219
177      Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro
178          15 20 25
180      CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT      267
181      Pro Pro Glu Glu Asp Pro Glu Glu Asp Ser Gly Pro Glu Asp Leu Pro
182          30 35 40
184      CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA      315
185      Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
186          45 50 55
188      TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG      363
189      Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
190          60 65 70 75
192      TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT      411
193      Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
194          80 85 90
196      ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA      459
197      Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
198          95 100 105
200      GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC      507
201      Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
202          110 115 120
204      ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT      555
205      Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
206          125 130 135
208      ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT      603
209      Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
210          140 145 150 155
212      GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT      651
213      Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
214          160 165 170
216      ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT      699
217      Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser
218          175 180 185
220      GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG      747
221      Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly
222          190 195 200
224      GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG      795

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225	Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	
226		205				210						215					
228	CTA	TGT	GTC	CTT	GAC	TAT	TTT	ATT	AAA	CTC	TCA	CCT	CCC	ATG	TTG	CTC	843
229	Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	
230	220					225					230					235	
232	AAA	GAA	CCA	TAT	AAA	ACA	GCT	GTT	ATA	CCC	ATT	AAT	GGT	TCA	CCT	CGA	891
233	Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	
234					240					245					250		
236	ACA	CCC	AGG	CGA	GGT	CAG	AAC	AGG	AGT	GCA	CGG	ATA	GCA	AAA	CAA	CTA	939
237	Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	
238					255				260					265			
240	GAA	AAT	GAT	ACA	AGA	ATT	ATT	GAA	GTT	CTC	TGT	AAA	GAA	CAT	GAA	TGT	987
241	Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	
242			270					275					280				
244	AAT	ATA	GAT	GAG	GTG	AAA	AAT	GTT	TAT	TTC	AAA	AAT	TTT	ATA	CCT	TTT	1035
245	Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	
246		285					290				295						
248	ATG	AAT	TCT	CTT	GGA	CTT	GTA	ACA	TCT	AAT	GGA	CTT	CCA	GAG	GTT	GAA	1083
249	Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	
250	300				305					310					315		
252	AAT	CTT	TCT	AAA	CGA	TAC	GAA	GAA	ATT	TAT	CTT	AAA	AAT	AAA	GAT	CTA	1131
253	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	
254				320					325					330			
256	GAT	GCA	AGA	TTA	TTT	TTG	GAT	CAT	GAT	AAA	ACT	CTT	CAG	ACT	GAT	TCT	1179
257	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	
258			335						340					345			
260	ATA	GAC	AGT	TTT	GAA	ACA	CAG	AGA	ACA	CCA	CGA	AAA	AGT	AAC	CTT	GAT	1227
261	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	
262			350					355					360				
264	GAA	GAG	GTG	AAT	GTA	ATT	CTT	CCA	CAC	ACT	CCA	GTT	AGG	ACT	GTT	ATG	1275
265	Glu	Glu	Val	Asn	Val	Ile	Leu	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	
266		365				370					375						
268	AAC	ACT	ATC	CAA	CAA	TTA	ATG	ATG	ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	1323
269	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	
270	380				385					390					395		
272	CCT	TCA	GAA	AAT	CTG	ATT	TCC	TAT	TTT	AAC	AAC	TGC	ACA	GTG	AAT	CCA	1371
273	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	
274				400						405				410			
276	AAA	GAA	AGT	ATA	CTG	AAA	AGA	GTG	AAG	GAT	ATA	GGA	TAC	ATC	TTT	AAA	1419
277	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	
278			415					420					425				
280	GAG	AAA	TTT	GCT	AAA	GCT	GTG	GGA	CAG	GGT	TGT	GTC	GAA	ATT	GGA	TCA	1467
281	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	
282			430					435					440				
284	CAG	CGA	TAC	AAA	CTT	GGA	GTT	CGC	TTG	TAT	TAC	CGA	GTA	ATG	GAA	TCC	1515
285	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	
286		445					450						455				
288	ATG	CTT	AAA	TCA	GAA	GAA	GAA	CGA	TTA	TCC	ATT	CAA	AAT	TTT	AGC	AAA	1563
289	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	

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290	460				465				470				475				
292	CTT	CTG	AAT	GAC	AAC	ATT	TTT	CAT	ATG	TCT	TTA	TTG	GCG	TGC	GCT	CTT	1611
293	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	
294					480					485					490		
296	GAG	GTT	GTA	ATG	GCC	ACA	TAT	AGC	AGA	AGT	ACA	TCT	CAG	AAT	CTT	GAT	1659
297	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	
298				495					500					505			
300	TCT	GGA	ACA	GAT	TTG	TCT	TTC	CCA	TGG	ATT	CTG	AAT	GTG	CTT	AAT	TTA	1707
301	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	
302				510					515				520				
304	AAA	GCC	TTT	GAT	TTT	TAC	AAA	GTG	ATC	GAA	AGT	TTT	ATC	AAA	GCA	GAA	1755
305	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	
306		525					530				535						
308	GGC	AAC	TTG	ACA	AGA	GAA	ATG	ATA	AAA	CAT	TTA	GAA	CGA	TGT	GAA	CAT	1803
309	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	
310	540					545					550				555		
312	CGA	ATC	ATG	GAA	TCC	CTT	GCA	TGG	CTC	TCA	GAT	TCA	CCT	TTA	TTT	GAT	1851
313	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	
314				560					565				570				
316	CTT	ATT	AAA	CAA	TCA	AAG	GAC	CGA	GAA	GGA	CCA	ACT	GAT	CAC	CTT	GAA	1899
317	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	
318			575				580				585						
320	TCT	GCT	TGT	CCT	CTT	AAT	CTT	CCT	CTC	CAG	AAT	AAT	CAC	ACT	GCA	GCA	1947
321	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	
322		590					595				600						
324	GAT	ATG	TAT	CTT	TCT	CCT	GTA	AGA	TCT	CCA	AAG	AAA	AAA	GGT	TCA	ACT	1995
325	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	
326		605				610					615						
328	ACG	CGT	GTA	AAT	TCT	ACT	GCA	AAT	GCA	GAG	ACA	CAA	GCA	ACC	TCA	GCC	2043
329	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	
330	620				625					630					635		
332	TTC	CAG	ACC	CAG	AAG	CCA	TTG	AAA	TCT	ACC	TCT	CTT	TCA	CTG	TTT	TAT	2091
333	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	
334				640					645				650				
336	AAA	AAA	GTG	TAT	CGG	CTA	GCC	TAT	CTC	CGG	CTA	AAT	ACA	CTT	TGT	GAA	2139
337	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	
338			655				660				665						
340	CGC	CTT	CTG	TCT	GAG	CAC	CCA	GAA	TTA	GAA	CAT	ATC	ATC	TGG	ACC	CTT	2187
341	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	
342		670					675				680						
344	TTC	CAG	CAC	ACC	CTG	CAG	AAT	GAG	TAT	GAA	CTC	ATG	AGA	GAC	AGG	CAT	2235
345	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	
346		685				690					695						
348	TTG	GAC	CAA	ATT	ATG	ATG	TGT	TCC	ATG	TAT	GGC	ATA	TGC	AAA	GTG	AAG	2283
349	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	
350	700				705					710					715		
352	AAT	ATA	GAC	CTT	AAA	TTC	AAA	ATC	ATT	GTA	ACA	GCA	TAC	AAG	GAT	CTT	2331
353	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	
354				720					725						730		

VERIFICATION SUMMARY

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L:29 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:220 C: Keyword misspelled or invalid format, (A) APPLICATION NUMBER:
L:36 M:220 C: Keyword misspelled or invalid format, (B) FILING DATE:
L:39 M:220 C: Keyword misspelled or invalid format, (A) APPLICATION NUMBER:
L:40 M:220 C: Keyword misspelled or invalid format, (B) FILING DATE:
L:60 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1, Value=[DNA]
L:76 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2, Value=[DNA]
L:92 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3, Value=[DNA]
L:108 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4, Value=[DNA]
L:124 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5, Value=[DNA]
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